

Application No.: 89462416

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/462,416

DATE: 07/30/2001  
TIME: 14:57:53

Input Set : A:\PTO\_VSK.txt  
Output Set: N:\CRF3\07302001\I462416.raw

3 <110> APPLICANT: REVEL, Michel  
4 CHEBATH, Judith  
5 LAPIDOT, Tsvee  
6 KOLLET, Orit  
8 <120> TITLE OF INVENTION: CHIMERIC INTERLEUKIN-6 SOLUBLE RECEPTOR/LIGAND PROTEIN,  
ANALOGS THEREOF  
9 AND USES THEREOF  
11 <130> FILE REFERENCE: REVEL=15  
13 <140> CURRENT APPLICATION NUMBER: 09/462,416  
14 <141> CURRENT FILING DATE: 2000-04-13  
16 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00321  
17 <151> PRIOR FILING DATE: 1998-07-09  
19 <150> PRIOR APPLICATION NUMBER: IL 121284  
20 <151> PRIOR FILING DATE: 1997-07-10  
22 <150> PRIOR APPLICATION NUMBER: IL 122818  
23 <151> PRIOR FILING DATE: 1997-12-30  
25 <160> NUMBER OF SEQ ID NOS: 12  
27 <170> SOFTWARE: PatentIn version 3.1  
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31 <212> TYPE: PRT  
32 <213> ORGANISM: Artificial Sequence  
34 <220> FEATURE:  
35 <223> OTHER INFORMATION: synthetic  
37 <400> SEQUENCE: 1  
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40 1 5 10  
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44 <211> LENGTH: 22  
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48 <220> FEATURE:  
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58 <213> ORGANISM: Artificial Sequence  
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67 <210> SEQ ID NO: 4  
68 <211> LENGTH: 21  
69 <212> TYPE: DNA  
70 <213> ORGANISM: Artificial Sequence  
72 <220> FEATURE:

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 116 1 5 10 15  
 119 Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg  
 120 20 25 30  
 123 Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro  
 124 35 40 45  
 127 Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys  
 128 50 55 60  
 131 Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg  
 132 65 70 75 80  
 135 Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys  
 136 85 90 95  
 139 Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val  
 140 100 105 110  
 143 Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser  
 144 115 120 125  
 147 Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr  
 148 130 135 140  
 151 Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp  
 152 145 150 155 160  
 155 Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys  
 156 165 170 175

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159 Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met  
 160 180 185 190  
 163 Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe  
 164 195 200 205  
 167 Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val  
 168 210 215 220  
 171 Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp  
 172 225 230 235 240  
 175 Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg  
 176 245 250 255  
 179 Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp  
 180 260 265 270  
 183 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His  
 184 275 280 285  
 187 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser  
 188 290 295 300  
 191 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser  
 192 305 310 315 320  
 195 Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr  
 196 325 330 335  
 199 Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr  
 200 340 345 350  
 203 Ser Leu Pro Val Glu Phe Met Pro Val Pro Pro Gly Glu Asp Ser Lys  
 204 355 360 365  
 207 Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile  
 208 370 375 380  
 211 Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys  
 212 385 390 395 400  
 215 Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu  
 216 405 410 415  
 219 Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys  
 220 420 425 430  
 223 Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr  
 224 435 440 445  
 227 Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe  
 228 450 455 460  
 231 Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val  
 232 465 470 475 480  
 235 Leu Ile Gln Phe Leu Gln Lys Ala Lys Asn Leu Asp Ala Ile Thr  
 236 485 490 495  
 239 Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala  
 240 500 505 510  
 243 Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser  
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 248 530 535 540  
 251 <210> SEQ ID NO: 8  
 252 <211> LENGTH: 471  
 253 <212> TYPE: PRT

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254 <213> ORGANISM: Artificial Sequence  
 256 <220> FEATURE:  
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 266 20 25 30  
 269 Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr  
 270 35 40 45  
 273 Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile  
 274 50 55 60  
 277 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser  
 278 65 70 75 80  
 281 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala  
 282 85 90 95  
 285 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu  
 286 100 105 110  
 289 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr  
 290 115 120 125  
 293 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln  
 294 130 135 140  
 297 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn  
 298 145 150 155 160  
 301 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu  
 302 165 170 175  
 305 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His  
 306 180 185 190  
 309 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala  
 310 195 200 205  
 313 Leu Arg Gln Met Gly Gly Gly Asp Pro Gly Gly Gly Gly Gly Gly  
 314 210 215 220  
 317 Pro Gly Val Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser  
 318 225 230 235 240  
 321 Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser  
 322 245 250 255  
 325 Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro  
 326 260 265 270  
 329 Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys  
 330 275 280 285  
 333 Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile  
 334 290 295 300  
 337 Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr  
 338 305 310 315 320  
 341 Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn  
 342 325 330 335  
 345 Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr  
 346 340 345 350  
 349 Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe

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350	355	360	365
353	Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met		
354	370	375	380
357	Val Lys Asp Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly		
358	385	390	395
361	Leu Arg His Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly		400
362	405	410	415
365	Glu Trp Ser Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu		
366	420	425	430
369	Ser Arg Ser Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala		
370	435	440	445
373	Leu Thr Thr Asn Lys Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala		
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423	<223> OTHER INFORMATION: synthetic		
425	<400> SEQUENCE: 12		
426	gatccccgccc accccggggcc ca		22

VERIFICATION SUMMARY

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